

Replacement SheetFIG. 1A

Met	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Cys	Ala	Val	Leu	Ala	Leu	Ser	His	1	5	10	15
Thr	Ala	Asn	Pro	Cys	Cys	Ser	His	Pro	Cys	Gln	Asn	Arg	Gly	Val	Cys	20	25	30	
Met	Ser	Val	Gly	Phe	Asp	Gln	Tyr	Lys	Cys	Asp	Cys	Thr	Arg	Thr	Gly	35	40	45	
Phe	Tyr	Gly	Glu	Asn	Cys	Ser	Thr	Pro	Glu	Phe	Leu	Thr	Arg	Ile	Lys	50	55	60	
Leu	Phe	Leu	Lys	Pro	Thr	Pro	Asn	Thr	Val	His	Tyr	Ile	Leu	Thr	His	65	70	75	80
Phe	Lys	Gly	Phe	Trp	Asn	Val	Val	Asn	Asn	Ile	Pro	Phe	Leu	Arg	Asn	85	90	95	
Ala	Ile	Met	Ser	Tyr	Val	Leu	Thr	Ser	Arg	Ser	His	Leu	Ile	Asp	Ser	100	105	110	
Pro	Pro	Thr	Tyr	Asn	Ala	Asp	Tyr	Gly	Tyr	Lys	Ser	Trp	Glu	Ala	Phe	115	120	125	
Ser	Asn	Leu	Ser	Tyr	Tyr	Thr	Arg	Ala	Leu	Pro	Pro	Val	Pro	Asp	Asp	130	135	140	
Cys	Pro	Thr	Pro	Leu	Gly	Val	Lys	Gly	Lys	Lys	Gln	Leu	Pro	Asp	Ser	145	150	155	160
Asn	Glu	Ile	Val	Glu	Lys	Leu	Leu	Leu	Arg	Arg	Lys	Phe	Ile	Pro	Asp	165	170	175	
Pro	Gln	Gly	Ser	Asn	Met	Met	Phe	Ala	Phe	Phe	Ala	Gln	His	Phe	Thr	180	185	190	
His	Gln	Phe	Phe	Lys	Thr	Asp	His	Lys	Arg	Gly	Pro	Ala	Phe	Thr	Asn	195	200	205	
Gly	Leu	Gly	His	Gly	Val	Asp	Leu	Asn	His	Ile	Tyr	Gly	Glu	Thr	Leu	210	215	220	
Ala	Arg	Gln	Arg	Lys	Leu	Arg	Leu	Phe	Lys	Asp	Gly	Lys	Met	Lys	Tyr	225	230	235	240
Gln	Ile	Ile	Asp	Gly	Glu	Met	Tyr	Pro	Pro	Thr	Val	Lys	Asp	Thr	Gln	245	250	255	
Ala	Glu	Met	Ile	Tyr	Pro	Pro	Gln	Val	Pro	Glu	His	Leu	Arg	Phe	Ala	260	265	270	
Val	Gly	Gln	Glu	Val	Phe	Gly	Leu	Val	Pro	Gly	Leu	Met	Met	Tyr	Ala	275	280	285	
Thr	Ile	Trp	Leu	Arg	Glu	His	Asn	Arg	Val	Cys	Asp	Val	Leu	Lys	Gln	290	295	300	

Replacement SheetFIG 1B

Glu	His	Pro	Glu	Trp	Gly	Asp	Glu	Gln	Leu	Phe	Gln	Thr	Ser	Arg	Leu	305	310	315	320
Ile	Leu	Ile	Gly	Glu	Thr	Ile	Lys	Ile	Val	Ile	Glu	Asp	Tyr	Val	Gln	325	330	335	
His	Leu	Ser	Gly	Tyr	His	Phe	Lys	Leu	Lys	Phe	Asp	Pro	Glu	Leu	Leu	340	345	350	
Phe	Asn	Lys	Gln	Phe	Gln	Tyr	Gln	Asn	Arg	Ile	Ala	Ala	Glu	Phe	Asn	355	360	365	
Thr	Leu	Tyr	His	Trp	His	Pro	Leu	Leu	Pro	Asp	Thr	Phe	Gln	Ile	His	370	375	380	
Asp	Gln	Lys	Tyr	Asn	Tyr	Gln	Gln	Phe	Ile	Tyr	Asn	Asn	Ser	Ile	Leu	385	390	395	400
Leu	Glu	His	Gly	Ile	Thr	Gln	Phe	Val	Glu	Ser	Phe	Thr	Arg	Gln	Ile	405	410	415	
Ala	Gly	Arg	Val	Ala	Gly	Gly	Arg	Asn	Val	Pro	Pro	Ala	Val	Gln	Lys	420	425	430	
Val	Ser	Gln	Ala	Ser	Ile	Asp	Gln	Ser	Arg	Gln	Met	Lys	Tyr	Gln	Ser	435	440	445	
Phe	Asn	Glu	Tyr	Arg	Lys	Arg	Phe	Met	Leu	Lys	Pro	Tyr	Glu	Ser	Phe	450	455	460	
Glu	Glu	Leu	Thr	Gly	Glu	Lys	Glu	Met	Ser	Ala	Glu	Leu	Glu	Ala	Leu	465	470	475	480
Tyr	Gly	Asp	Ile	Asp	Ala	Val	Glu	Leu	Tyr	Pro	Ala	Leu	Leu	Val	Glu	485	490	495	
Lys	Pro	Arg	Pro	Asp	Ala	Ile	Phe	Gly	Glu	Thr	Met	Val	Glu	Val	Gly	500	505	510	
Ala	Pro	Phe	Ser	Leu	Lys	Gly	Leu	Met	Gly	Asn	Val	Ile	Cys	Ser	Pro	515	520	525	
Ala	Tyr	Trp	Lys	Pro	Ser	Thr	Phe	Gly	Gly	Glu	Val	Gly	Phe	Gln	Ile	530	535	540	
Ile	Asn	Thr	Ala	Ser	Ile	Gln	Ser	Leu	Ile	Cys	Asn	Asn	Val	Lys	Gly	545	550	555	560
Cys	Pro	Phe	Thr	Ser	Phe	Ser	Val	Pro	Asp	Pro	Glu	Leu	Ile	Lys	Thr	565	570	575	
Val	Thr	Ile	Asn	Ala	Ser	Ser	Ser	Arg	Ser	Gly	Leu	Asp	Asp	Ile	Asn	580	585	590	
Pro	Thr	Val	Leu	Leu	Lys	Glu	Arg	Ser	Thr	Glu	Leu	(SEQ ID NO: 10)				595	600		

Replacement SheetFIG. 2B

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CTCAATTCAG TCTCTCATCT GCAATAACGT GAAGGGCTGT CCCTTTACTT CATTTCAGTGT 1800
TCCAGATCCA GAGCTCATT A AACAGTCAC CATCAATGCA AGTTCTTCCC GCTCCGGACT 1860
AGATGATATC AATCCCACAG TACTACTAAA AGAACGGTCG ACTGAACTGT AGAAGTCTAA 1920
TGATCATATT TATTTATTTA TATGAACCAT GTCTATTAAT TTAATTATTT AATAATATTT 1980
ATATTAAACT CCTTATGTTA CTTAACATCT TCTGTAACAG AAGTCAGTAC TCCTGTTGCG 2040
GAGAAAGGAG TCATACTTGT GAAGACTTTT ATGTCACTAC TCTAAAGATT TTGCTGTTGC 2100
TGTTAAGTTT GGAAAACAGT TTTTATTCTG TTTTATAAAC CAGAGAGAAA TGAGTTTGA 2160
CGTCTTTTTT CTTGAATTTT AACTTATATT ATAAGGACGA AAGTAAAGAT GTTTGAATAC 2220
TTAAACACTA TCACAAGATG CCAAATGCT GAAAGTTTTT ACCTGTCTGA TGTTTCCAAT 2280
GCATCTTCCA TGATGCATTA GAAGTAACTA ATGTTTGAAA TTTTAAAGTA CTTTGGGTA 2340
TTTTTCTGTC ATCAAACAAA ACAGGTATCA GTGCATTATT AAATGAATAT TTAAATTAGA 2400
CATTACCAGT AATTCATGT CTACTTTTTT AAATCAGCAA TGAAACAATA ATTTGAAATT 2460
TCTAAATTCA TAGGGTAGAA TCACCTGTAA AAGCTTGTTT GATTTCTTAA AGTTATTAAA 2520
CTTGACATA TACCAAAAAG AAGCTGTCTT GGATTTAAAT CTGTAAATC AGATGAAATT 2580
TTACTACAAT TGCTTGTTAA AATATTTTAT AAGTGATGTT CCTTTTTCAC CAAGAGTATA 2640
AACCTTTTTT GTGTGACTGT TAAACTTCC TTTTAAATCA AAATGCCAAA TTTATTAAGG 2700
TGGTGGAGCC ACTGCAGTGT TATCTCAAAA TAAGAATATC CTGTTGAGAT ATTCCAGAAT 2760
CTGTTTATAT GGCTGGTAAC ATGTAAAAAC CCCATAACCC CGCCAAAAGG GGTCTACCC 2820
TTGAACATAA AGCAATAACC AAAGGAGAAA AGCCCAAATT ATTGGTTCCA AATTTAGGGT 2880
TTAAACTTTT TGAAGCAAAC TTTTTTTTAG CCTGTGCAC TGCAGACCTG GACTCAGAT 2940
TTTGCTATGA GGTAAATGAA GTACCAAGCT GTGCTTGAAT AACGATATGT TTTCTCAGAT 3000
TTTCTGTTGT ACAGTTTAAT TTAGCAGTCC ATATCACATT GCAAAAGTAG CAATGACCTC 3060
ATAAAATACC TCTTCAAAT GCTTAAATC ATTTACACA TTAATTTTAT CTCAGTCTTG 3120
AAGCCAATTC AGTAGGTGCA TTGGAATCAA GCCTGGCTAC CTGCATGCTG TTCCTTTTCT 3180
TTTCTTCTTT TAGCCATTTT GCTAAGAGAC ACAGTCTTCT CAAACACTTC GTTCTCCTA 3240
TTTTGTTTTA CTAGTTTTAA GATCAGAGTT CACTTTCTTT GGACTCTGCC TATATTTTCT 3300
TACCTGAAC TTTGCAAGTT TTCAGGTAAA CCTCAGCTCA GGACTGCTAT TTAGCTCCTC 3360
TTAAGAAGAT TAAAAAAG AAAAAAG (SEQ ID NO: 11) 3387

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